

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/876,187B
Source: FW16
Date Processed by STIC: 6/26/06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 06/26/2006

PATENT APPLICATION: US/09/876,187B

TIME: 10:31:09

Input Set : A:\66654-622.TAT

Output Set: N:\CRF4\06262006\I876187B.raw

4 <110> APPLICANT: Lipton, Stuart A.
 5 Okamoto, Shu-ichi
 7 <120> TITLE OF INVENTION: Methods of Differentiating and
 8 Protecting Cells By Modulating the P38/MEF2 Pathway
 11 <130> FILE REFERENCE: 66654-622
 13 <140> CURRENT APPLICATION NUMBER: US 09/876,187B
 14 <141> CURRENT FILING DATE: 2001-06-05
 16 <150> PRIOR APPLICATION NUMBER: US 60/209,539
 17 <151> PRIOR FILING DATE: 2000-06-05
 19 <160> NUMBER OF SEQ ID NOS: 25
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 2975
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (415)...(1935)
 32 <400> SEQUENCE: 1
 33 gaattttctg caaggatcat atctaagtgc actttttgct gatacttcat ttctagacat 60
 34 tgagtctcac tctaccccc aggctgaagt gcagtggtgt gatctcgggt cactgcaacc 120
 35 tccgcctcca ggttcaagtg attctcgtac ctcagcctcc cgagtagctg ggattacagg 180
 36 cgccctgccac catgcctggc tgatatttat attttttagta gagatggagt ttcaccatgt 240
 37 tggccaggct ggtctcgaac tctggacctc agatcttgta gaaaatttca gctgtagccc 300
 38 ttggactaga agctgaaata acagaagctg tgtacgatgc attagggtat tgaagaaaat 360
 39 taacttttga attaaatatt tggaatataa ggaaataagg aaagttgact gaaa atg 417
 40 Met
 41 1
 43 ggg cgg aag aaa ata caa atc aca cgc ata atg gat gaa agg aac cga 465
 44 Gly Arg Lys Lys Ile Gln Ile Thr Arg Ile Met Asp Glu Arg Asn Arg
 45 5 10 15
 47 cag gtc act ttt aca aag aga aag ttt gga tta atg aag aaa gcc tat 513
 48 Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala Tyr
 49 20 25 30
 51 gaa ctt agt gtg ctc tgt gac tgt gaa ata gca ctc atc att ttc aac 561
 52 Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe Asn
 53 35 40 45
 55 agc tct aac aaa ctg ttt caa tat gct agc act gat atg gac aaa gtt 609
 56 Ser Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys Val
 57 50 55 60 65
 59 ctt ctc aag tat aca gaa tat aat gaa cct cat gaa agc aga acc aac 657
 60 Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr Asn
 61 70 75 80

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63 tcg gat att gtt gag gct ctg aac aag aag gaa cac aga ggg tgc gac 705
64 Ser Asp Ile Val Glu Ala Leu Asn Lys Lys Glu His Arg Gly Cys Asp
65      85      90      95
67 agc cca gac cct gat act tca tat gtg cta act cca cat aca gaa gaa 753
68 Ser Pro Asp Pro Asp Thr Ser Tyr Val Leu Thr Pro His Thr Glu Glu
69      100      105      110
71 aaa tat aaa aat att aat ggg gaa ttt gat aat atg atg cgg aat cat 801
72 Lys Tyr Lys Lys Ile Asn Glu Glu Phe Asp Asn Met Met Arg Asn His
73      115      120      125
75 aaa atc gca cct ggt ctg cca cct cag aac ttt tca atg tct gtc aca 849
76 Lys Ile Ala Pro Gly Leu Pro Pro Gln Asn Phe Ser Met Ser Val Thr
77 130      135      140      145
79 gtt cca gtg acc agc ccc aat gct ttg tcc tac act aac cca ggg agt 897
80 Val Pro Val Thr Ser Pro Asn Ala Leu Ser Tyr Thr Asn Pro Gly Ser
81      150      155      160
83 tca ctg gtg tcc cca tct ttg gca gcc agc tca acg tta aca gat tca 945
84 Ser Leu Val Ser Pro Ser Leu Ala Ala Ser Ser Thr Leu Thr Asp Ser
85      165      170      175
87 agc atg ctc tct cca cct caa acc aca tta cat aga aab gtg tct cct 993
88 Ser Met Leu Ser Pro Pro Gln Thr Thr Leu His Arg Asn Val Ser Pro
89      180      185      190
91 gga gct cct cag aga cca cca agt act ggc aat gca ggt ggg atg ttg 1041
92 Gly Ala Pro Gln Arg Pro Pro Ser Thr Gly Asn Ala Gly Gly Met Leu
93      195      200      205
95 agc act aca gac ctc aca gtg cca aat gga gct gga agc agt cca gtg 1089
96 Ser Thr Thr Asp Leu Thr Val Pro Asn Gly Ala Gly Ser Ser Pro Val
97 210      215      220      225
99 ggg aat gga ttt gta aac tca aga gct tct cca aat ttg att gga gct 1137
100 Gly Asn Gly Phe Val Asn Ser Arg Ala Ser Pro Asn Leu Ile Gly Ala
101      230      235      240
103 act ggt gca aat agc tta ggc aaa gtc atg cct aca aag tct ccc cct 1185
104 Thr Gly Ala Asn Ser Leu Gly Lys Val Met Pro Thr Lys Ser Pro Pro
105      245      250      255
107 cca cca ggt ggt ggt aat ctt gga atg aac agt agg aaa cca gat ctt 1233
108 Pro Pro Gly Gly Gly Asn Leu Gly Met Asn Ser Arg Lys Pro Asp Leu
109      260      265      270
111 cga gtt gtc atc ccc cct tca agc aag ggc atg atg cct cca cta tcg 1281
112 Arg Val Val Ile Pro Pro Ser Ser Lys Gly Met Met Pro Pro Leu Ser
113      275      280      285
115 gag gaa gag gaa ttg gag ttg aac acc caa agg atc agt agt tct caa 1329
116 Glu Glu Glu Glu Leu Glu Leu Asn Thr Gln Arg Ile Ser Ser Ser Gln
117 290      295      300      305
119 gcc act caa cct ctt gct acc cca gtc gtg tct gtg aca acc cca agc 1377
120 Ala Thr Gln Pro Leu Ala Thr Pro Val Val Ser Val Thr Thr Pro Ser
121      310      315      320
123 ttg cct ccg caa gga ctt gtg tac tca gca atg ccg act gcc tac aac 1425
124 Leu Pro Pro Gln Gly Leu Val Tyr Ser Ala Met Pro Thr Ala Tyr Asn
125      325      330      335
127 act gat tat tca ctg acc agc gct gac ctg tca gcc ctt caa ggc ttc 1473

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128 Thr Asp Tyr Ser Leu Thr Ser Ala Asp Leu Ser Ala Leu Gln Gly Phe
129      340      345      350
131 aac tcg cca gga atg ctg tcg ctg gga cag gtg tcg gcc tgg cag cag 1521
132 Asn Ser Pro Gly Met Leu Ser Leu Gly Gln Val Ser Ala Trp Gln Gln
133      355      360      365
135 cac cac cta gga caa gca gcc ctg agc tct ctt gtt gct gga ggg cag 1569
136 His His Leu Gly Gln Ala Ala Leu Ser Ser Leu Val Ala Gly Gly Gln
137 370      375      380      385
139 tta tct cag ggt tcc aat tta tcc att aat acc aac caa aac atc agc 1617
140 Leu Ser Gln Gly Ser Asn Leu Ser Ile Asn Thr Asn Gln Asn Ile Ser
141      390      395      400
143 atc aag tcc gaa ccg att tca cct cct cgg gat cgt atg acc cca tcg 1665
144 Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg Met Thr Pro Ser
145      405      410      415
147 ggc ttc cag cag cag cag cag cag cag cag cag cag cag ccg ccg cca 1713
148 Gly Phe Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro
149      420      425      430
151 cca ccg cag ccc cag cca caa ccc ccg cag ccc cag ccc cga cag gaa 1761
152 Pro Ser Gln Pro Gln Pro Gln Pro Pro Gln Pro Gln Pro Arg Gln Glu
153      435      440      445
155 atg ggg cgc tcc cct gtg gac agt ctg agc agc tct agt agc tcc tat 1809
156 Met Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Ser Ser Ser Ser Tyr
157 450      455      460      465
159 gat ggc agt gat cgg gag gat cca cgg ggc gac ttc cat tct cca att 1857
160 Asp Gly Ser Asp Arg Glu Asp Pro Arg Gly Asp Phe His Ser Pro Ile
161      470      475      480
163 gtg ctt ggc cga ccc cca aac act gag gac aga gaa agc cct tct gta 1905
164 Val Leu Gly Arg Pro Pro Asn Thr Glu Asp Arg Glu Ser Pro Ser Val
165      485      490      495
167 aag cga atg agg atg gac gcg tgg gtg acc taaggcttcc aagctgatgt 1955
168 Lys Arg Met Arg Met Asp Ala Trp Val Thr
169      500      505
171 ttgtactttt gtgttactgc agtgacctgc cctacatatc taaatcggtg aataaggaca 2015
172 tgagttaaata atatttatat gtacatacat atatatatcc ctttacatat atatgtatgt 2075
173 ggggtgtgagt gtgtgtgtat gtgtgggtgt gtgttacata cacagaatca ggcacttacc 2135
174 tgcaaaactcc ttgtaggtct gcagatgtgt gtcccatggc agacaaaagca ccctgtaggc 2195
175 acagacaagt ctggcacttc cttggactac ttgtttcgta aagataacca gtttttgcag 2255
176 agaaacgtgt acccatatat aattctccca cactagcttg cagaaaccta gagggccccc 2315
177 tacttgtttt atttaactgt gcagtgactg tagttactta agagaaaatg cttttagtaa 2375
178 cagagcagta gaaaagcagg aaccaagaaa gcaatactgt acataaaatg tcatttatat 2435
179 tttccaacct ggcattgggtg tctgttgcaa aggggtgcat gggaaagggc tgttgatatt 2495
180 aaaaacaaac aaaacaaaaa agccccacac ataactgttt tgcacgtgca aaaatgtatt 2555
181 gggtaagaa gtgatcttta gctaataaag aaagagaata gaaaacacgc atgagatatt 2615
182 cagaaaatac tagcctagaa atatagagca ttaacaaagg aaaattaata tattaagtta 2675
183 taattggaat atgtcagaag tttcttttta cattcatatc ttaaaaatta aagaaactga 2735
184 ttttagctca tgtatatattt atatgaaaga aaacaccctt atgaattgat gactatatat 2795
185 aaaattatat tcaactattt tgaacacatt ctgctatgaa ttatttatat aagccaaagc 2855
186 tatatgttgt aacttttttt tagagaatag ctttatcttg gtttaactct ttagttttat 2915
187 ttaagaggg gaaaacaaaa atatcttgca agcagaacct tgaaaaaaa aaaggaattc 2975

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190 <210> SEQ ID NO: 2
191 <211> LENGTH: 507
192 <212> TYPE: PRT
193 <213> ORGANISM: Homo sapiens
195 <400> SEQUENCE: 2
196 Met Gly Arg Lys Lys Ile Gln Ile Thr Arg Ile Met Asp Glu Arg Asn
197 1 5 10 15
198 Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala
199 20 25 30
200 Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
201 35 40 45
202 Asn Ser Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
203 50 55 60
204 Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
205 65 70 75 80
206 Asn Ser Asp Ile Val Glu Ala Leu Asn Lys Lys Glu His Arg Gly Cys
207 85 90 95
208 Asp Ser Pro Asp Pro Asp Thr Ser Tyr Val Leu Thr Pro His Thr Glu
209 100 105 110
210 Glu Lys Tyr Lys Lys Ile Asn Glu Phe Asp Asn Met Met Arg Asn
211 115 120 125
212 His Lys Ile Ala Pro Gly Leu Pro Pro Gln Asn Phe Ser Met Ser Val
213 130 135 140
214 Thr Val Pro Val Thr Ser Pro Asn Ala Leu Ser Tyr Thr Asn Pro Gly
215 145 150 155 160
216 Ser Ser Leu Val Ser Pro Ser Leu Ala Ala Ser Ser Thr Leu Thr Asp
217 165 170 175
218 Ser Ser Met Leu Ser Pro Pro Gln Thr Thr Leu His Arg Asn Val Ser
219 180 185 190
220 Pro Gly Ala Pro Gln Arg Pro Pro Ser Thr Gly Asn Ala Gly Gly Met
221 195 200 205
222 Leu Ser Thr Thr Asp Leu Thr Val Pro Asn Gly Ala Gly Ser Ser Pro
223 210 215 220
224 Val Gly Asn Gly Phe Val Asn Ser Arg Ala Ser Pro Asn Leu Ile Gly
225 225 230 235 240
226 Ala Thr Gly Ala Asn Ser Leu Gly Lys Val Met Pro Thr Lys Ser Pro
227 245 250 255
228 Pro Pro Pro Gly Gly Gly Asn Leu Gly Met Asn Ser Arg Lys Pro Asp
229 260 265 270
230 Leu Arg Val Val Ile Pro Pro Ser Ser Lys Gly Met Met Pro Pro Leu
231 275 280 285
232 Ser Glu Glu Glu Glu Leu Glu Leu Asn Thr Gln Arg Ile Ser Ser Ser
233 290 295 300
234 Gln Ala Thr Gln Pro Leu Ala Thr Pro Val Val Ser Val Thr Thr Pro
235 305 310 315 320
236 Ser Leu Pro Pro Gln Gly Leu Val Tyr Ser Ala Met Pro Thr Ala Tyr
237 325 330 335
238 Asn Thr Asp Tyr Ser Leu Thr Ser Ala Asp Leu Ser Ala Leu Gln Gly
239 340 345 350

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240 Phe Asn Ser Pro Gly Met Leu Ser Leu Gly Gln Val Ser Ala Trp Gln
241           355                      360                      365
242 Gln His His Leu Gly Gln Ala Ala Leu Ser Ser Leu Val Ala Gly Gly
243           370                      375                      380
244 Gln Leu Ser Gln Gly Ser Asn Leu Ser Ile Asn Thr Asn Gln Asn Ile
245 385                      390                      395                      400
246 Ser Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg Met Thr Pro
247           405                      410                      415
248 Ser Gly Phe Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro
249           420                      425                      430
250 Pro Pro Pro Gln Pro Gln Pro Gln Pro Pro Gln Pro Gln Pro Arg Gln
251           435                      440                      445
252 Glu Met Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Ser Ser Ser Ser
253           450                      455                      460
254 Tyr Asp Gly Ser Asp Arg Glu Asp Pro Arg Gly Asp Phe His Ser Pro
255 465                      470                      475                      480
256 Ile Val Leu Gly Arg Pro Pro Asn Thr Glu Asp Arg Glu Ser Pro Ser
257           485                      490                      495
258 Val Lys Arg Met Arg Met Asp Ala Trp Val Thr
259           500                      505
262 <210> SEQ ID NO: 3
263 <211> LENGTH: 1671
264 <212> TYPE: DNA
265 <213> ORGANISM: Homo sapiens
267 <220> FEATURE:
268 <221> NAME/KEY: CDS
269 <222> LOCATION: (443)...(1537)
271 <400> SEQUENCE: 3
272 cggggggtcgc tatggaggag ccggagatgc agctcaaggg gaagaaagtc acggacaagt 60
273 tcaactgagag cgtctacgtc ctggccaacg agccatccgt ggccctgtac cggctgcagg 120
274 agcatgtgcg tcgctccctc cccgagctgg ccagcacaa ggagacatg cagcgttggg 180
275 aggagcagag ccagggagcc atctacactg tggagtacgc ctgcagcgcc gtgaagaacc 240
276 tgggtggacag cagcgtctac ttccgcagcg tggagggtct gctcaaacag gccatcagca 300
277 tccgggacca tatgaatgcc agtgcccagg gccacagccc ggaggaacca ccccgccct 360
278 cctcagcctg atcctggaag agactcgggg ccccccagcc tccgccaacc cagacaaaga 420
279 tcattccact cagcctggga cg atg ggg agg aaa aaa atc cag atc tcc cgc 472
280           Met Gly Arg Lys Lys Ile Gln Ile Ser Arg
281           1                      5                      10
283 atc ctg gac caa agg aat cgg cag gtg acg ttc acc aag cgg aag ttc 520
284 Ile Leu Asp Gln Arg Asn Arg Gln Val Thr Phe Thr Lys Arg Lys Phe
285           15                      20                      25
287 ggg ctg atg aag aag gcc tat gag ctg agc gtg ctc tgt gac tgt gag 568
288 Gly Leu Met Lys Lys Ala Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu
289           30                      35                      40
291 ata gcc ctc atc atc ttc aac agc gcc aac cgc ctc ttc cag tat gcc 616
292 Ile Ala Leu Ile Ile Phe Asn Ser Ala Asn Arg Leu Phe Gln Tyr Ala
293           45                      50                      55
295 agc acg gac atg gac cgt gtg ctg ctg aag tac aca gag tac agc gag 664
296 Ser Thr Asp Met Asp Arg Val Leu Leu Lys Tyr Thr Glu Tyr Ser Glu

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; Xaa Pos. 9,10,11,12,13,14,15,16,17

Seq#:17; Xaa Pos. 9,10,11,12,13,14

Seq#:21; Xaa Pos. 9,10,11,12,13,14,15,16,17,18

VERIFICATION SUMMARY

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Input Set : A:\66654-622.TXT

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L:953 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:955 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:16
L:1006 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:1059 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:1061 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:16